

SEQUENCE LISTING

<110> ALBANI, SALVATORE

<120> METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION
AND MODULATION OF ANTIGEN-SPECIFIC T CELLS

<130> AND-TCCICIP1-DIV2

<140>

<141>

<150> 09/756,983

<151> 2001-01-09

<150> PCT/US99/24666

<151> 1999-10-19

<150> 09/421,506

<151> 1999-10-19

<150> 60/105,018

<151> 1998-10-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from third hyper V region of IE molecule of Mus musculus

<400> 1

Ala	Ser	Phe	Glu	Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys
1				5				10						15	

Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from bole I protein of Epstein Barr virus

<400> 2

Thr	Arg	Asp	Asp	Ala	Glu	Tyr	Leu	Leu	Gly	Arg	Glu	Ser	Val	Leu
1				5					10					15

<210> 3
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the haemophilus influenza virus

<400> 3
 Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
 1 5 10 15

<210> 4
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the TCR receptor of Mus musculus

<220>
 <221> MOD_RES
 <222> (18)
 <223> Ser, Ile or Thr

<400> 4
 Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys
 1 5 10 15

Ala Xaa Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro
 20 25 30

Gly Thr Arg Leu
 35

<210> 5
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the influenza virus

<400> 5
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 6

Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 7

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (2)

<223> cyclohexylalanine

<400> 7

Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala
1 5 10

<210> 8

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 8

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 9

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial

<400> 9

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

Arg

<210> 10
 <211> 15
 <212> PRT
 <213> Escherichia coli

<400> 10
 Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
 1 5 10 15

<210> 11
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 11
 Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
 1 5 10 15

<210> 12
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 12
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 13
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 13
 Val Lys Leu Gly Glu Phe Tyr Asn Gln
 1 5

<210> 14
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 14
 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
 1 5 10

<210> 15
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct with
 human and bacterial sequences

<220>

<221> CDS

<222> (1)..(939)

<400> 15

atg ggc cac aca cgg agg cag gga aca tca cca tcc aag tgt cca tac	48
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr	
1 5 10 15	
ctc aat ttc ttt cag ctc ttg gtg ctg gct ggt ctt tct cac ttc tgt	96
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys	
20 25 30	
tca ggt gtt atc cac gtg acc aag gaa gtg aaa gaa gtg gca acg ctg	144
Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu	
35 40 45	
tcc tgt ggt cac aat gtt tct gtt gaa gag ctg gca caa act cgc atc	192
Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile	
50 55 60	
tac tgg caa aag gag aag aaa atg gtg ctg act atg atg tct ggg gac	240
Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp	
65 70 75 80	
atg aat ata tgg ccc gag tac aag aac cgg acc atc ttt gat atc act	288
Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr	
85 90 95	
aat aac ctc tcc att gtg atc ctg gct ctg cgc cca tct gac gag ggc	336
Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly	
100 105 110	
aca tac gag tgt gtt gtt ctg aag tat gaa aaa gac gct ttc aag cgg	384
Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg	
115 120 125	
gaa cac ctg gct gaa gtg acg tta tca gtc aaa gct gac ttc cct aca	432
Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr	
130 135 140	
cct agt ata tct gac ttt gaa att cca act tct aat att aga agg ata	480
Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile	
145 150 155 160	
att tgc tca acc tct gga ggt ttt cca gag cct cac ctc tcc tgg ttg	528
Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu	
165 170 175	
gaa aat gga gaa gaa tta aat gcc atc aac aca aca gtt tcc caa gat	576
Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp	
180 185 190	
cct gaa act gag ctc tat gct gtt agc gaa ttc ggc ggc tcc ggt ggt	624
Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly	
195 200 205	

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agc gcc aca cct caa aat att act gat ttg tgt gca gaa tac cac aac 672
Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
210 215 220

aca caa ata cat acg cta aat gat aag ata ttt tcg tat aca gaa tct 720
Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
225 230 235 240

cta gct gga aaa aga gag atg gct atc att act ttt aag aat ggt gca 768
Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
245 250 255

act ttt caa gta gaa gta cca ggt agt caa cat ata gat tca caa aaa 816
Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
260 265 270

aaa gcg att gaa agg atg aag gat acc ctg agg att gca tat ctt act 864
Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
275 280 285

gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa acg cct cat 912
Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
290 295 300

gcg att gcc gca att agt atg gca aat taa 942
Ala Ile Ala Ala Ile Ser Met Ala Asn
305 310

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<210> 16

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 16

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Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

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Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
    100                                105                    110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
    115                                120                    125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
    130                                135                    140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
    145                                150                    155                    160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
    165                                170                    175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
    180                                185                    190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly
    195                                200                    205

Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
    210                                215                    220

Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
    225                                230                    235                    240

Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
    245                                250                    255

Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
    260                                265                    270

Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
    275                                280                    285

Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
    290                                295                    300

Ala Ile Ala Ala Ile Ser Met Ala Asn
    305                                310

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<210> 17

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<220>

<221> CDS

<222> (1)..(1053)

<400> 17

atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg ctc tct ggt	48
Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly	
1 5 10 15	
gct gct cct ctg aag att caa gct tat ttc aat gag act gca gac ctg	96
Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu	
20 25 30	
cca tgc caa ttt gca aac tct caa aac caa agc ctg agt gag cta gta	144
Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val	
35 40 45	
gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag gta tac tta	192
Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu	
50 55 60	
ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg ggc cgc aca	240
Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr	
65 70 75 80	
agt ttt gat tcg gac agt tgg acc ctg aga ctt cac aat ctt cag atc	288
Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile	
85 90 95	
aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa aag ccc aca	336
Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr	
100 105 110	
gga atg att cgc atc cac cag atg aat tct gaa ctg tca gtg ctt gct	384
Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala	
115 120 125	
aac ttc agt caa cct gaa ata gta cca att tct aat ata aca gaa aat	432
Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn	
130 135 140	
gtg tac ata aat ttg acc tgc tca tct ata cac ggt tac cca gaa cct	480
Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro	
145 150 155 160	
aag aag atg agt gtt ttg cta aga acc aag aat tca act atc gag tat	528
Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr	
165 170 175	
gat ggt att atg cag aaa tct caa gat aat gtc aca gaa ctg tac gac	576
Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp	
180 185 190	
gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg	624
Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met	
195 200 205	
acc atc ttc tgt att ctg gaa act gac aag acg cgg ctt tta tct tca	672
Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser	
210 215 220	


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cct ttc tct ata gag ctt gag gac cct cag cct ccc cca gac cac gaa 720
Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
225                230                235                240

ttc ggc ggc tcc ggt ggt agc gcc aca cct caa aat att act gat ttg 768
Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
                245                250                255

tgt gca gaa tac cac aac aca caa ata cat acg cta aat gat aag ata 816
Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
                260                265                270

ttt tcg tat aca gaa tct cta gct gga aaa aga gag atg gct atc att 864
Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
                275                280                285

act ttt aag aat ggt gca act ttt caa gta gaa gta cca ggt agt caa 912
Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
                290                295                300

cat ata gat tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg 960
His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
305                310                315                320

agg att gca tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg 1008
Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
                325                330                335

aat aat aaa acg cct cat gcg att gcc gca att agt atg gca aat taa 1056
Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
                340                345                350

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<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 18

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Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
 1                5                10                15

Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
                20                25                30

Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
                35                40                45

Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
 50                55                60

Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
65                70                75                80

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Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	Leu	His	Asn	Leu	Gln	Ile	85	90	95
Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	His	His	Lys	Lys	Pro	Thr	100	105	110
Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser	Val	Leu	Ala	115	120	125
Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile	Thr	Glu	Asn	130	135	140
Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr	Pro	Glu	Pro	145	150	155
Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	Ile	Glu	Tyr	165	170	175
Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	Tyr	Asp	180	185	190
Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	Ser	Asn	Met	195	200	205
Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	Leu	Ser	Ser	210	215	220
Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	Asp	His	Glu	225	230	235
Phe	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Thr	Pro	Gln	Asn	Ile	Thr	Asp	Leu	245	250	255
Cys	Ala	Glu	Tyr	His	Asn	Thr	Gln	Ile	His	Thr	Leu	Asn	Asp	Lys	Ile	260	265	270
Phe	Ser	Tyr	Thr	Glu	Ser	Leu	Ala	Gly	Lys	Arg	Glu	Met	Ala	Ile	Ile	275	280	285
Thr	Phe	Lys	Asn	Gly	Ala	Thr	Phe	Gln	Val	Glu	Val	Pro	Gly	Ser	Gln	290	295	300
His	Ile	Asp	Ser	Gln	Lys	Lys	Ala	Ile	Glu	Arg	Met	Lys	Asp	Thr	Leu	305	310	315
Arg	Ile	Ala	Tyr	Leu	Thr	Glu	Ala	Lys	Val	Glu	Lys	Leu	Cys	Val	Trp	325	330	335
Asn	Asn	Lys	Thr	Pro	His	Ala	Ile	Ala	Ala	Ile	Ser	Met	Ala	Asn		340	345	350

<210> 19

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 19

Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala
 1 5 10 15

Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
 20 25 30

<210> 20

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 20

Ala Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln
 1 5 10 15

Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
 20 25 30

<210> 21

<211> 1095

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(1092)

<400> 21

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 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1 5 10 15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96
 Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
 20 25 30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144
 Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60

gag	acg	gtc	tgg	cgg	ctt	gaa	gaa	ttt	gga	cga	ttt	gcc	agc	ttt	gag	240
Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	Phe	Ala	Ser	Phe	Glu	
65					70					75					80	
gct	caa	ggt	gca	ttg	gcc	aac	ata	gct	gtg	gac	aaa	gcc	aac	ctg	gaa	288
Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu	
				85					90					95		
atc	atg	aca	aag	cgc	tcc	aac	tat	act	ccg	atc	acc	aat	gta	cct	cca	336
Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro	
			100					105					110			
gag	gta	act	gtg	ctc	acg	aac	agc	cct	gtg	gaa	ctg	aga	gag	ccc	aac	384
Glu	Val	Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn	
		115					120					125				
gtc	ctc	atc	tgt	ttc	atc	gac	aag	ttc	acc	cca	cca	gtg	gtc	aat	gtc	432
Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val	
	130					135						140				
acg	tgg	ctt	cga	aat	gga	aaa	cct	gtc	acc	aca	gga	gtg	tca	gag	aca	480
Thr	Trp	Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr	
145					150					155					160	
gtc	ttc	ctg	ccc	agg	gaa	gac	cac	ctt	ttc	cgc	aag	ttc	cac	tat	ctc	528
Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu	
				165					170					175		
ccc	ttc	ctg	ccc	tca	act	gag	gac	gtt	tac	gac	tgc	agg	gtg	gag	cac	576
Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His	
			180					185					190			
tgg	ggc	ttg	gat	gag	cct	ctt	ctc	aag	cac	tgg	gag	ttt	gat	gct	cca	624
Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	
		195					200					205				
agc	cct	ctc	cca	gag	act	aca	gag	gaa	ttc	ggc	ggc	tcc	ggc	ggc	tcc	672
Ser	Pro	Leu	Pro	Glu	Thr	Thr	Glu	Glu	Phe	Gly	Gly	Ser	Gly	Gly	Ser	
	210					215						220				
gcg	cag	ctg	gaa	tgg	gaa	ctg	cag	gcg	ctg	gaa	aaa	gaa	aac	gcg	cag	720
Ala	Gln	Leu	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	Asn	Ala	Gln	
225					230					235					240	
ctg	gaa	tgg	gaa	ctg	cag	gcg	ctg	gaa	aaa	gaa	ctg	gcg	cag	ggc	ggc	768
Leu	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	Leu	Ala	Gln	Gly	Gly	
				245					250					255		
tcc	ggc	ggc	agc	gcc	aca	cct	caa	aat	att	act	gat	ttg	tgt	gca	gaa	816
Ser	Gly	Gly	Ser	Ala	Thr	Pro	Gln	Asn	Ile	Thr	Asp	Leu	Cys	Ala	Glu	
			260					265					270			
tac	cac	aac	aca	caa	ata	cat	acg	cta	aat	gat	aag	ata	ttt	tcg	tat	864
Tyr	His	Asn	Thr	Gln	Ile	His	Thr	Leu	Asn	Asp	Lys	Ile	Phe	Ser	Tyr	
		275					280					285				

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aca gaa tct cta gct gga aaa aga gag atg gct atc att act ttt aag 912
Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
    290                295                300

aat ggt gca act ttt caa gta gaa gta cca ggt agt caa cat ata gat 960
Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
    305                310                315                320

tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg agg att gca 1008
Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
    325                330                335

tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa 1056
Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
    340                345                350

acg cct cat gcg att gcc gca att agt atg gca aat taa 1095
Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
    355                360

```

<210> 22

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 22

```

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
  1              5              10              15

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
    20              25              30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
    35              40              45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
    50              55              60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
    65              70              75              80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
    85              90              95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
    100             105             110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
    115             120             125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
    130             135             140

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Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145                      150                      155                      160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
                      165                      170                      175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
                      180                      185                      190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195                      200                      205

Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
210                      215                      220

Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
225                      230                      235                      240

Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
245                      250                      255

Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
260                      265                      270

Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
275                      280                      285

Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
290                      295                      300

Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
305                      310                      315                      320

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
325                      330                      335

Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
340                      345                      350

Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
355                      360

```

<210> 23

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(855)

<400> 23

atg gtg tgt ctg aag ttc cct gga ggc tcc tgc atg gca gct ctg aca	48
Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr	
1 5 10 15	
gtg aca ctg atg gtg ctg agc tcc cca ctg gct ttg gct ggg gac acc	96
Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr	
20 25 30	
cga cca cgt ttc ttg gag cag gtt aaa cat gag tgt cat ttc ttc aac	144
Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn	
35 40 45	
ggg acg gag cgg gtg cgg ttc ctg gac aga tac ttc tat cac caa gag	192
Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu	
50 55 60	
gag tac gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtg acg	240
Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr	
65 70 75 80	
gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc	288
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu	
85 90 95	
ctg gag cag aag cgg gcc gcg gtg gac acc tac tgc aga cac aac tac	336
Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr	
100 105 110	
ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtc tat cct gag gtg	384
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val	
115 120 125	
act gtg tat cct gca aag acc cag ccc ctg cag cac cac aac ctc ctg	432
Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu	
130 135 140	
gtc tgc tct gtg aat ggt ttc tat cca ggc agc att gaa gtc agg tgg	480
Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp	
145 150 155 160	
ttc cgg aac ggc cag gaa gag aag act ggg gtg gtg tcc aca ggc ctg	528
Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu	
165 170 175	
atc cag aat gga gac tgg acc ttc cag acc ctg gtg atg ctg gaa aca	576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr	
180 185 190	
gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agc	624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	
195 200 205	
ctg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca	672
Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	
210 215 220	

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cag agc aag ggc ggc tcc ggt ggt agc gcc cag ctg aag aag aaa ctc 720
Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
225                230                235                240

cag gct ctg aaa aaa aag aat gcc cag ctc aag cag aag ctg cag gcc 768
Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
                245                250                255

ctg aag aaa aag ctg gct cag ggt tcc ggt ggt tcc gcg ggt ggt ggt 816
Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
                260                265                270

ttg aac gac atc ttc gaa gct cag aaa atc gaa tgg cac taataa 861
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
                275                280                285

```

<210> 24

<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 24

```

Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr
 1                5                10                15

Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr
                20                25                30

Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn
 35                40                45

Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
 50                55                60

Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
 65                70                75                80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
                85                90                95

Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr
                100                105                110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
                115                120                125

Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
                130                135                140

Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145                150                155                160

```


Phe	Arg	Asn	Gly	Gln	Glu	Glu	Lys	Thr	Gly	Val	Val	Ser	Thr	Gly	Leu
			165						170					175	
Ile	Gln	Asn	Gly	Asp	Trp	Thr	Phe	Gln	Thr	Leu	Val	Met	Leu	Glu	Thr
			180					185					190		
Val	Pro	Arg	Ser	Gly	Glu	Val	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Ser
		195					200					205			
Leu	Thr	Ser	Pro	Leu	Thr	Val	Glu	Trp	Arg	Ala	Arg	Ser	Glu	Ser	Ala
	210					215					220				
Gln	Ser	Lys	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Gln	Leu	Lys	Lys	Lys	Leu
225					230					235					240
Gln	Ala	Leu	Lys	Lys	Lys	Asn	Ala	Gln	Leu	Lys	Gln	Lys	Leu	Gln	Ala
			245					250						255	
Leu	Lys	Lys	Lys	Leu	Ala	Gln	Gly	Ser	Gly	Gly	Ser	Ala	Gly	Gly	Gly
			260					265					270		
Leu	Asn	Asp	Ile	Phe	Glu	Ala	Gln	Lys	Ile	Glu	Trp	His			
	275						280					285			